



Links

11/17/03 10:55 AM

sections only once, except for a short overlap.
The true left end of clone RP4-585I14 is at 84023 in this sequence.
The true right end of clone RP5-1077I2 is at 100 in this sequence.

FEATURES
Location/Qualifiers

source 1..84122
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP11-149I18"
/clone_lib="RPCI-11.1"

gene 1..30067
/gene="C20orf82"

mRNA join(<1..159,9050..9314,17956..18099,21790..21879,
28358..30067)
/gene="C20orf82"
/product="bA149I18.1 (novel protein)"
/note="Continues from dJ1077I2.1 in Em:AL050320
match: ESTs: Em:AI191256 Em:R44763 Em:W86073 Em:AI082824
Em:AI886394 Em:R52250 Em:AV708785 Em:W07772 Em:AV660737
Em:BF302850 Em:AW426875 Em:W86257 Em:AW873508 Em:BE287313
Em:AW495535 Em:AW435648 Em:AW435639 Em:AL732076"
/evidence=not_experimental

CDS join(<1..159,9050..9314,17956..18099,21790..21879,
28358..28875)
/gene="C20orf82"
/note="Continues from dJ1077I2.1 in Em:AL050320
match: proteins: Tr:Q9H599 Tr:O95432"
/codon_start=1
/evidence=not_experimental
/product="bA149I18.1 (novel protein)"
/protein_id="CAC16127.2"
/db_xref="GI:13374941"
/db_xref="GOA:Q9H599"
/db_xref="SPTREMBL:Q9H599"
/translation="HQA AHQPFP RPRFRQETGHP SLQRDFPRS FLDDL PNF PDLSKAD
INGQNPNIQVTIEVVDGPDSEADKDQHPENKPSWSVSPDWRAWQRSLSLARANS
GDQDYKDSTSDSNFLNPPRGWDHTAPGHRTFETKDQPEYDSTDGEGDWSLWSVCSVTC
GNGNQKRTRSCGYACTATESRTCDRPNCPGIEDTFRTAATEVSLLAGSEEFNATKLFE
VDTDSCERWMSCKSEFLKKYMHKVMNDLPSCPCSYPTVAYSTADIFDRIKRKDFRWK
DASGPKEKLEIYKPTARYCIRSMLSLESTTLAAQHCCYGDNMQLITRGKGAGTPNLIS
TEFSAELHYKVDVLPWIICKGDWSRYNEARPPNNGQKCTESPSDEDYIKQFQEAREY"

repeat region complement(316..456)
/note="MER104 repeat: matches 32..176 of consensus"

repeat region 453..472
/note="4.0 copies 5 mer AAAAC 31% conserved"

repeat region 487..505
/note="3.8 copies 5 mer AAAAC 38% conserved"

repeat region 708..717
/note="2.5 copies 4 mer AGGA 20% conserved"

repeat region complement(885..1058)
/note="MIR repeat: matches 24..189 of consensus"

repeat region complement(1202..1494)
/note="AluJb repeat: matches 1..289 of consensus"

repeat region 2597..2608
/note="2.0 copies 6 mer ATTCCC 24% conserved"

repeat region 2632..2670
/note="7.8 copies 5 mer TTTTA 78% conserved"

repeat region complement(2642..2951)
/note="AluJo repeat: matches 1..311 of consensus"

repeat region 3417..3426
/note="2.5 copies 4 mer AAAG 20% conserved"

repeat region 3476..3501
/note="13.0 copies 2 mer TG 43% conserved"

repeat region 3498..3511

<u>repeat region</u>	/note="2.3 copies 6 mer TGTGCA 28% conserved" 3512..3538
<u>repeat region</u>	/note="13.5 copies 2 mer CA 29% conserved" 3950..3967
<u>repeat region</u>	/note="2.2 copies 8 mer CCTCCCCA 27% conserved" 4082..4106
<u>repeat region</u>	/note="5.0 copies 5 mer CCCCCG 25% conserved" 4908..5154
<u>repeat region</u>	/note="MIR repeat: matches 34..238 of consensus" 5194..5205
<u>repeat region</u>	/note="2.0 copies 6 mer AGATGA 24% conserved" 5203..5333
<u>repeat region</u>	/note="MIR3 repeat: matches 2..145 of consensus" 6382..6398
<u>repeat region</u>	/note="3.4 copies 5 mer TGTTT 25% conserved" 6560..6569
<u>repeat region</u>	/note="10.0 copies 1 mer A 20% conserved" 7020..7033
<u>repeat region</u>	/note="2.0 copies 7 mer GATGTAT 28% conserved" 7036..7048
<u>repeat region</u>	/note="2.6 copies 5 mer CTTTT 26% conserved" 7060..7073
<u>repeat region</u>	/note="14.0 copies 1 mer T 28% conserved" 7507..7606
<u>repeat region</u>	/note="MER121 repeat: matches 167..268 of consensus" 7867..7878
<u>repeat region</u>	/note="2.0 copies 6 mer CACCTG 24% conserved" 7941..8067
<u>repeat region</u>	/note="MIR repeat: matches 1..140 of consensus" complement(8078..8523)
<u>repeat region</u>	/note="MLT1H1 repeat: matches 27..527 of consensus" 8373..8385
<u>repeat region</u>	/note="2.2 copies 6 mer AATGAA 26% conserved" 8538..8624
<u>repeat region</u>	/note="MIR repeat: matches 170..262 of consensus" 8680..8796
<u>repeat region</u>	/note="MLT1H1 repeat: matches 395..518 of consensus" 8840..8849
<u>repeat region</u>	/note="2.0 copies 5 mer CCCAA 20% conserved" 9512..9528
<u>repeat region</u>	/note="3.4 copies 5 mer AAATC 25% conserved" 9751..9760
<u>repeat region</u>	/note="2.0 copies 5 mer AGTGG 20% conserved" 9808..9819
<u>repeat region</u>	/note="12.0 copies 1 mer C 24% conserved" complement(9887..10266)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 6..416 of consensus" complement(10536..10673)
<u>repeat region</u>	/note="L2 repeat: matches 3125..3270 of consensus" complement(10826..11052)
<u>repeat region</u>	/note="MIR repeat: matches 2..261 of consensus" 11277..11343
<u>repeat region</u>	/note="MER5A repeat: matches 35..101 of consensus" 11344..11517
<u>repeat region</u>	/note="MER5A repeat: matches 1..182 of consensus" 11367..11381
<u>repeat region</u>	/note="2.5 copies 6 mer CCAGAA 21% conserved" 11520..11698
<u>repeat region</u>	/note="MER5B repeat: matches 2..178 of consensus" 11773..11825
<u>repeat region</u>	/note="MER5A repeat: matches 136..187 of consensus" 11978..11989
<u>repeat region</u>	/note="2.0 copies 6 mer CCTAGA 24% conserved" complement(12156..12212)
<u>repeat region</u>	/note="MER5A repeat: matches 132..189 of consensus"

<u>repeat region</u>	complement(12248..12291) /note="MER5A repeat: matches 9..52 of consensus"
<u>repeat region</u>	12306..12348 /note="L2 repeat: matches 3271..3313 of consensus"
<u>repeat region</u>	12337..12350 /note="3.5 copies 4 mer GAAT 28% conserved"
<u>repeat region</u>	complement(12443..12595) /note="FRAM repeat: matches 1..40 of consensus"
<u>repeat region</u>	12453..12464 /note="3.0 copies 4 mer TTTA 24% conserved"
<u>repeat region</u>	12686..12700 /note="2.5 copies 6 mer GAAACA 21% conserved"
<u>repeat region</u>	12995..13005 /note="2.2 copies 5 mer AGATG 22% conserved"
<u>repeat region</u>	13397..13552 /note="MIR repeat: matches 35..193 of consensus"
<u>repeat region</u>	14129..14138 /note="2.5 copies 4 mer ACAT 20% conserved"
<u>repeat region</u>	14157..14167 /note="2.2 copies 5 mer TTCAC 22% conserved"
<u>repeat region</u>	complement(14382..14420) /note="MLT1H repeat: matches 516..549 of consensus"
<u>repeat region</u>	14418..14428 /note="2.2 copies 5 mer CCAGG 22% conserved"
<u>repeat region</u>	14421..14739 /note="AluJo repeat: matches 1..310 of consensus"
<u>repeat region</u>	14712..14739 /note="28.0 copies 1 mer A 20% conserved"
<u>repeat region</u>	complement(14740..15136) /note="MLT1H repeat: matches 27..516 of consensus"
<u>repeat region</u>	14796..14826 /note="3.1 copies 10 mer GTCTGGACTG 35% conserved"
<u>repeat region</u>	14807..14826 /note="4.0 copies 5 mer TCTGG 31% conserved"
<u>repeat region</u>	14830..14841 /note="2.0 copies 6 mer GGCTGG 24% conserved"
<u>repeat region</u>	16323..16332 /note="3.3 copies 3 mer GCA 20% conserved"
<u>repeat region</u>	complement(16534..16892) /note="THE1B repeat: matches 1..364 of consensus"
<u>repeat region</u>	16900..17163 /note="L2 repeat: matches 3054..3310 of consensus"
<u>repeat region</u>	17154..17163 /note="2.5 copies 4 mer TGGA 20% conserved"
<u>repeat region</u>	complement(17207..17419) /note="MLT1H1 repeat: matches 327..555 of consensus"
<u>repeat region</u>	17381..17399 /note="1.9 copies 10 mer AGAAGGCTTG 38% conserved"
<u>repeat region</u>	17573..17596 /note="12.0 copies 2 mer TC 32% conserved"
<u>repeat region</u>	18197..18215 /note="3.8 copies 5 mer CTTTT 31% conserved"
<u>repeat region</u>	complement(18198..18489) /note="AluSg repeat: matches 13..301 of consensus"
<u>repeat region</u>	18198..18218 /note="21.0 copies 1 mer T 24% conserved"
<u>repeat region</u>	18871..18882 /note="2.4 copies 5 mer AAAC 24% conserved"
<u>repeat region</u>	18940..19047 /note="MER58C repeat: matches 1..132 of consensus"
<u>repeat region</u>	19015..19028 /note="4.7 copies 3 mer GAA 21% conserved"
<u>repeat region</u>	19016..19034 /note="3.2 copies 6 mer AAGAGA 22% conserved"
<u>repeat region</u>	19034..19043

<u>repeat region</u>	/note="3.3 copies 3 mer AGG 20% conserved" 19040..19117
<u>repeat region</u>	/note="6.5 copies 12 mer AGGAGGAAGAGA 56% conserved" 19050..19061
<u>repeat region</u>	/note="2.0 copies 6 mer GAAGGG 24% conserved" 19065..19115
<u>repeat region</u>	/note="17.0 copies 3 mer GGA 66% conserved" 19103..19197
<u>repeat region</u>	/note="MER58C repeat: matches 119..215 of consensus" 19679..19694
<u>repeat region</u>	/note="5.3 copies 3 mer GAG 23% conserved" 19785..20098
<u>repeat region</u>	/note="AluY repeat: matches 2..306 of consensus" 20083..20097
<u>repeat region</u>	/note="3.8 copies 4 mer AAAG 30% conserved" 20121..20131
<u>repeat region</u>	/note="2.2 copies 5 mer AAAAT 22% conserved" 20132..20142
<u>repeat region</u>	/note="3.7 copies 3 mer GAT 22% conserved" complement(20136..20382)
<u>repeat region</u>	/note="MIR repeat: matches 8..261 of consensus" 20797..20807
<u>repeat region</u>	/note="2.2 copies 5 mer CCTGG 22% conserved" 20968..20977
<u>repeat region</u>	/note="3.3 copies 3 mer CCT 20% conserved" complement(21260..21460)
<u>repeat region</u>	/note="MIR repeat: matches 2..219 of consensus" 21417..21426
<u>repeat region</u>	/note="2.5 copies 4 mer CAGT 20% conserved" 21536..21546
<u>repeat region</u>	/note="2.8 copies 4 mer AGTG 22% conserved" 21933..21945
<u>repeat region</u>	/note="2.2 copies 6 mer CTTTTG 26% conserved" 21973..21988
<u>repeat region</u>	/note="2.7 copies 6 mer TTTCAT 23% conserved" 22015..22024
<u>repeat region</u>	/note="2.5 copies 4 mer CTTG 20% conserved" 22257..22270
<u>repeat region</u>	/note="3.5 copies 4 mer GAGG 28% conserved" 22331..22644
<u>repeat region</u>	/note="AluY repeat: matches 1..302 of consensus" 22579..22596
<u>repeat region</u>	/note="2.2 copies 8 mer GCACTCCA 36% conserved" 22624..22641
<u>repeat region</u>	/note="18.0 copies 1 mer A 36% conserved" 22744..22759
<u>repeat region</u>	/note="2.3 copies 7 mer AGGTGCA 32% conserved" 22920..22930
<u>repeat region</u>	/note="11.0 copies 1 mer T 22% conserved" 22989..23014
<u>repeat region</u>	/note="2.0 copies 13 mer TGGGGTCAGGTAA 52% conserved" 23110..23419
<u>repeat region</u>	/note="AluSq repeat: matches 3..312 of consensus" 23316..23327
<u>repeat region</u>	/note="2.0 copies 6 mer GGAGGT 24% conserved" 23391..23424
<u>repeat region</u>	/note="34.0 copies 1 mer A 32% conserved" complement(23515..23680)
<u>repeat region</u>	/note="Charlie8 repeat: matches 29..199 of consensus" 23900..23910
<u>repeat region</u>	/note="2.8 copies 4 mer CAGG 22% conserved" complement(23996..24102)
<u>repeat region</u>	/note="LTR33 repeat: matches 415..521 of consensus" 24141..24155
<u>repeat region</u>	/note="2.5 copies 6 mer GCCACA 30% conserved"

repeat region complement(24208..24360)
/note="MIR repeat: matches 38..192 of consensus"
repeat region 24502..24512
/note="3.7 copies 3 mer CAC 22% conserved"
repeat region 24510..24526
/note="2.1 copies 8 mer CCAGCCTC 25% conserved"
repeat region 24858..24870
/note="2.2 copies 6 mer GCCCCA 26% conserved"
repeat region complement(24986..25364)
/note="LTR16B repeat: matches 1..449 of consensus"
repeat region 25471..25483
/note="2.2 copies 6 mer TTTGCC 26% conserved"
repeat region 25567..25576
/note="2.5 copies 4 mer ACCC 20% conserved"
repeat region 25584..25787
/note="LTR16C repeat: matches 11..241 of consensus"
repeat region complement(25792..26153)
/note="MER92B repeat: matches 272..631 of consensus"
repeat region 26154..26431
/note="AluSg repeat: matches 1..278 of consensus"
repeat region complement(26432..26701)
/note="MER92B repeat: matches 2..272 of consensus"
repeat region 26702..26928
/note="LTR16C repeat: matches 249..491 of consensus"
repeat region 26828..26843
/note="2.0 copies 8 mer TCCCCTGC 32% conserved"
repeat region complement(26967..27292)
/note="MER102b repeat: matches 5..329 of consensus"
repeat region 27020..27035
/note="3.2 copies 5 mer GAGCT 23% conserved"
repeat region 27483..27539
/note="14.2 copies 4 mer TTAT 46% conserved"
repeat region 27494..27516
/note="3.8 copies 6 mer TATTTT 37% conserved"
repeat region complement(27522..27831)
/note="AluSx repeat: matches 1..300 of consensus"
repeat region 27890..28097
/note="L1MC4 repeat: matches 7781..8042 of consensus"
repeat region 28355..28366
/note="2.0 copies 6 mer CAGACA 24% conserved"
repeat region 29140..29149
/note="3.3 copies 3 mer AGA 20% conserved"
repeat region 29346..29356
/note="2.8 copies 4 mer AGAA 22% conserved"
repeat region 29726..29736
/note="2.2 copies 5 mer AACAA 22% conserved"
repeat region 29814..29825
/note="3.0 copies 4 mer AATA 24% conserved"
polyA signal 29986..29991
/gene="C20orf82"
polyA site 30009
/gene="C20orf82"
repeat region 30044..30061
/note="6.0 copies 3 mer ATA 20% conserved"
polyA signal 30046..30051
/gene="C20orf82"
polyA signal 30057..30062
/gene="C20orf82"
polyA site 30067
/gene="C20orf82"
repeat region 30370..30381
/note="2.0 copies 6 mer CAATTA 24% conserved"
repeat region 30475..30484
/note="2.0 copies 5 mer CCTAG 20% conserved"
repeat region complement(30615..30902)

repeat region /note="AluSx repeat: matches 3..292 of consensus"
30615..30624
/note="10.0 copies 1 mer T 20% conserved"

repeat region 30846..30855
/note="2.5 copies 4 mer CTGC 20% conserved"

repeat region 30960..30972
/note="2.2 copies 6 mer ATATTT 26% conserved"

repeat region 31037..31047
/note="2.2 copies 5 mer TGAAC 22% conserved"

repeat region 31049..31205
/note="L3 repeat: matches 1315..1471 of consensus"

repeat region 31691..31701
/note="2.2 copies 5 mer GGAGG 22% conserved"

misc feature complement(31914..32511)
/note="match: GSS: Em:BH609834"

repeat region complement(32486..32620)
/note="MIR repeat: matches 18..153 of consensus"

repeat region 32635..32647
/note="2.6 copies 5 mer CTCTC 26% conserved"

misc feature 32941..33564
/note="match: GSS: Em:AG087240"

repeat region 33008..33102
/note="MIR repeat: matches 2..102 of consensus"

repeat region complement(33113..33228)
/note="L2 repeat: matches 3176..3313 of consensus"

repeat region complement(33296..33702)
/note="MLT1J2 repeat: matches 3..447 of consensus"

repeat region 34127..34395
/note="LTR16C repeat: matches 217..491 of consensus"

repeat region 34442..34468
/note="1.9 copies 14 mer TTAATATTTGATAT 54% conserved"

repeat region 34445..34468
/note="3.4 copies 7 mer ATATTTG 39% conserved"

repeat region complement(34614..34786)
/note="MER5C repeat: matches 1..204 of consensus"

repeat region 34616..34635
/note="20.0 copies 1 mer A 40% conserved"

repeat region 34922..34937
/note="2.3 copies 7 mer ATTTACA 23% conserved"

repeat region 35912..35939
/note="7.0 copies 4 mer TGTT 40% conserved"

repeat region 35964..35975
/note="2.0 copies 6 mer GGAGAA 24% conserved"

repeat region 35981..36002
/note="22.0 copies 1 mer A 44% conserved"

repeat region 36059..36068
/note="2.5 copies 4 mer TCAC 20% conserved"

repeat region 36134..36144
/note="2.2 copies 5 mer TGA CT 22% conserved"

repeat region complement(36698..36831)
/note="L1ME3A repeat: matches 6043..6165 of consensus"

repeat region 36832..36965
/note="L1ME1 repeat: matches 6011..6164 of consensus"

repeat region 36963..36972
/note="2.5 copies 4 mer AAAT 20% conserved"

repeat region complement(36986..37465)
/note="L1ME3A repeat: matches 5521..6021 of consensus"

repeat region complement(37559..37653)
/note="L2 repeat: matches 3144..3244 of consensus"

repeat region 37630..37641
/note="3.0 copies 4 mer AATG 24% conserved"

repeat region 37709..37725
/note="2.1 copies 8 mer ATGGGACC 25% conserved"

repeat region 37960..38052
/note="L1M4 repeat: matches 5719..5810 of consensus"

repeat region 38141..38497
/note="MLT1A repeat: matches 12..365 of consensus"

repeat region 38703..38713
/note="11.0 copies 1 mer A 22% conserved"

repeat region 38716..40318
/note="L1MA7 repeat: matches 3866..5480 of consensus"

repeat region 40328..40617
/note="AluSq repeat: matches 1..290 of consensus"

repeat region 40617..40629
/note="2.2 copies 6 mer ATAGAT 26% conserved"

repeat region 40623..40699
/note="19.2 copies 4 mer ATAG 140% conserved"

repeat region 40687..41480
/note="L1MA7 repeat: matches 5480..6287 of consensus"

repeat region 41051..41069
/note="1.9 copies 10 mer GAACATGGAT 29% conserved"

repeat region 41478..41487
/note="2.5 copies 4 mer AATT 20% conserved"

repeat region 41503..41512
/note="5.0 copies 2 mer AT 20% conserved"

repeat region 41680..41726
/note="2.2 copies 21 mer ATGTGAGTTCACAGCCGGCAT 76% conserved"

repeat region 41785..41798
/note="3.5 copies 4 mer ACTC 28% conserved"

repeat region 42030..42046
/note="2.1 copies 8 mer CTCTCCTG 34% conserved"

repeat region complement(42160..42306)
/note="MIR3 repeat: matches 6..166 of consensus"

repeat region 42598..42657
/note="L1MC1 repeat: matches 19..79 of consensus"

repeat region 42678..43070
/note="MER57A repeat: matches 8..403 of consensus"

repeat region 42947..42967
/note="1.9 copies 11 mer GCTGGAGTGTT 42% conserved"

repeat region 43071..45020
/note="L1MC1 repeat: matches 739..2835 of consensus"

repeat region 43352..43361
/note="2.5 copies 4 mer AAGA 20% conserved"

repeat region 43431..43445
/note="3.0 copies 5 mer GACTG 21% conserved"

repeat region 43526..43540
/note="3.0 copies 5 mer AACAG 21% conserved"

repeat region 43627..43637
/note="3.7 copies 3 mer AAT 22% conserved"

repeat region 43902..43911
/note="5.0 copies 2 mer GA 20% conserved"

repeat region 44229..44242
/note="2.3 copies 6 mer ATATCT 28% conserved"

repeat region 44236..44246
/note="2.8 copies 4 mer TATC 22% conserved"

repeat region 44319..44331
/note="2.2 copies 6 mer AGAATT 26% conserved"

repeat region 44794..44805
/note="2.0 copies 6 mer AGTAGC 24% conserved"

repeat region 45043..45427
/note="L1MC1 repeat: matches 2894..3283 of consensus"

repeat region 45361..45375
/note="2.5 copies 6 mer AAATGA 30% conserved"

repeat region 45428..48615
/note="L1MC1 repeat: matches 3487..6608 of consensus"

repeat region 45700..45710
/note="2.2 copies 5 mer AATTG 22% conserved"

repeat region 45705..45720
/note="2.3 copies 7 mer AATTAAT 23% conserved"

repeat region 45838..45847
/note="3.3 copies 3 mer ATT 20% conserved"

repeat region 45966..45976
/note="2.2 copies 5 mer CAAAT 22% conserved"

repeat region 46056..46066
/note="2.8 copies 4 mer AATT 22% conserved"

repeat region 46159..46170
/note="12.0 copies 1 mer A 24% conserved"

repeat region 46663..46686
/note="24.0 copies 1 mer A 21% conserved"

repeat region 46666..46684
/note="3.8 copies 5 mer AAAAC 38% conserved"

repeat region 47369..47380
/note="2.0 copies 6 mer ATTAAA 24% conserved"

repeat region 47553..47579
/note="6.8 copies 4 mer AAAT 54% conserved"

repeat region 47690..47699
/note="3.3 copies 3 mer ACA 20% conserved"

repeat region 48093..48116
/note="2.4 copies 10 mer GCTATCCAGT 39% conserved"

repeat region 48639..48649
/note="11.0 copies 1 mer A 22% conserved"

repeat region 48671..48681
/note="2.2 copies 5 mer CAAGG 22% conserved"

repeat region 48949..48974
/note="6.5 copies 4 mer AAAG 25% conserved"

repeat region 49032..49045
/note="3.5 copies 4 mer AAAC 21% conserved"

repeat region 49159..49169
/note="5.5 copies 2 mer CA 22% conserved"

repeat region 49196..49205
/note="2.5 copies 4 mer CAGC 20% conserved"

repeat region 49336..49347
/note="2.0 copies 6 mer ACAGGG 24% conserved"

repeat region 49684..49700
/note="2.1 copies 8 mer TTCCCAA 25% conserved"

repeat region 49881..49892
/note="2.4 copies 5 mer AAAAG 24% conserved"

repeat region complement(50138..50332)
/note="MLT1J repeat: matches 110..316 of consensus"

repeat region 50333..50631
/note="AluSx repeat: matches 1..296 of consensus"

repeat region complement(50632..50674)
/note="MLT1J repeat: matches 70..110 of consensus"

repeat region 50670..50692
/note="23.0 copies 1 mer A 46% conserved"

repeat region 50986..51107
/note="L2 repeat: matches 3200..3311 of consensus"

repeat region 51192..51203
/note="2.4 copies 5 mer TCTTT 24% conserved"

repeat region 51254..51496
/note="MIR repeat: matches 23..248 of consensus"

repeat region 51509..51520
/note="2.0 copies 6 mer AAGTAC 24% conserved"

misc feature complement(51715..51941)
/note="match: STS: Em:Z94397"

repeat region 52070..52083
/note="3.5 copies 4 mer ACAG 28% conserved"

repeat region 52943..52971
/note="1.9 copies 15 mer TTCAGTATGAACTA 42% conserved"

repeat region 53151..53165
/note="2.1 copies 7 mer AGTATTT 30% conserved"

repeat region 53181..53190
/note="3.3 copies 3 mer CTT 20% conserved"

repeat region 53481..53498

repeat region /note="2.0 copies 9 mer AGTAATTGC 27% conserved"
53889..53900

repeat region /note="2.0 copies 6 mer AATTTA 24% conserved"
53985..54005

repeat region /note="1.9 copies 11 mer TTAATCATGCC 33% conserved"
complement(54226..54316)

repeat region /note="MIR3 repeat: matches 93..183 of consensus"
54679..54692

repeat region /note="2.0 copies 7 mer AGGTCTC 28% conserved"
complement(55373..56126)

repeat region /note="L1ME1 repeat: matches 5301..6016 of consensus"
55768..55788

repeat region /note="3.5 copies 6 mer ATGTAT 33% conserved"
55800..55811

repeat region /note="2.0 copies 6 mer GTATAT 24% conserved"
55826..55837

repeat region /note="2.0 copies 6 mer GTATAT 24% conserved"
55862..55876

repeat region /note="2.5 copies 6 mer CCATCT 21% conserved"
55897..55906

repeat region /note="2.5 copies 4 mer CATA 20% conserved"
55900..55911

repeat region /note="2.0 copies 6 mer ACATAC 24% conserved"
56128..58383

repeat region /note="L1PA11 repeat: matches 3889..6164 of consensus"
57003..57014

repeat region /note="2.0 copies 6 mer TGGTAC 24% conserved"
57038..57049

repeat region /note="2.4 copies 5 mer GAACA 24% conserved"
58422..58442

repeat region /note="4.2 copies 5 mer AAAAT 33% conserved"
complement(58464..58568)

repeat region /note="L1ME1 repeat: matches 4385..4484 of consensus"
58465..58474

repeat region /note="2.5 copies 4 mer TTTC 20% conserved"
58569..58953

repeat region /note="MLT1B repeat: matches 5..390 of consensus"
complement(58954..59374)

repeat region /note="L1ME1 repeat: matches 3984..4385 of consensus"
58973..58988

repeat region /note="2.7 copies 6 mer TTTCAG 25% conserved"
59002..59013

repeat region /note="2.0 copies 6 mer TACAAA 24% conserved"
59144..59153

repeat region /note="10.0 copies 1 mer T 20% conserved"
complement(59375..59670)

repeat region /note="AluSx repeat: matches 1..296 of consensus"
59375..59386

repeat region /note="12.0 copies 1 mer T 24% conserved"
59554..59565

repeat region /note="2.0 copies 6 mer ATGGAG 24% conserved"
complement(59671..60619)

repeat region /note="L1ME1 repeat: matches 2944..3984 of consensus"
59751..59761

repeat region /note="2.8 copies 4 mer ATTG 22% conserved"
60398..60412

repeat region /note="3.8 copies 4 mer TTTG 30% conserved"
60724..60733

repeat region /note="2.5 copies 4 mer CAGA 20% conserved"
60854..60864

repeat region /note="2.2 copies 5 mer AATAG 22% conserved"
60964..60975

repeat region /note="2.0 copies 6 mer GGAGAA 24% conserved"
61069..61096

repeat region /note="2.3 copies 12 mer TTTTGGGGCTTT 38% conserved"

repeat region 61090..61104
/note="15.0 copies 1 mer T 30% conserved"

repeat region 61102..61142
/note="MLT1K repeat: matches 550..588 of consensus"

repeat region 61219..61270
/note="L2 repeat: matches 3148..3199 of consensus"

repeat region 61535..61555
/note="1.9 copies 11 mer GACAATGTTCT 35% conserved"

repeat region 61577..61586
/note="2.5 copies 4 mer TTAC 20% conserved"

repeat region complement(61638..62601)
/note="MER45B repeat: matches 4..1038 of consensus"

repeat region 61670..61681
/note="2.0 copies 6 mer AAAATG 24% conserved"

repeat region 62100..62114
/note="3.0 copies 5 mer GAAAA 30% conserved"

repeat region 62196..62214
/note="4.8 copies 4 mer TTCA 22% conserved"

repeat region 62650..62660
/note="2.2 copies 5 mer TTTGT 22% conserved"

repeat region 63923..63934
/note="2.0 copies 6 mer CATCTA 24% conserved"

repeat region 64159..64616
/note="HAL1 repeat: matches 2..462 of consensus"

repeat region 64516..64526
/note="2.2 copies 5 mer CACAG 22% conserved"

repeat region 64698..64708
/note="2.2 copies 5 mer TTCCC 22% conserved"

repeat region 64741..64787
/note="23.5 copies 2 mer CA 85% conserved"

repeat region 64797..64808
/note="2.0 copies 6 mer AGATTT 24% conserved"

repeat region 64975..64987
/note="3.2 copies 4 mer ATGA 26% conserved"

repeat region 65055..65549
/note="HAL1 repeat: matches 986..1516 of consensus"

repeat region 65205..65223
/note="3.2 copies 6 mer GCAAAA 29% conserved"

repeat region 65305..65318
/note="7.0 copies 2 mer AG 21% conserved"

repeat region 65589..65838
/note="MER45C repeat: matches 1..261 of consensus"

repeat region 65916..66134
/note="MER45C repeat: matches 706..953 of consensus"

misc feature complement(65987..66472)
/note="match: GSS: Em:AQ538453"

repeat region 66165..66174
/note="10.0 copies 1 mer T 20% conserved"

repeat region 66558..66719
/note="L3b repeat: matches 1406..1580 of consensus"

repeat region 67189..67200
/note="2.4 copies 5 mer AAGGA 24% conserved"

repeat region complement(67370..67969)
/note="MER41B repeat: matches 1..634 of consensus"

repeat region 67478..67494
/note="2.1 copies 8 mer TAAAAGAA 25% conserved"

repeat region 68298..68309
/note="2.0 copies 6 mer TCACCA 24% conserved"

repeat region 68299..68318
/note="2.2 copies 9 mer CACCATCAC 40% conserved"

repeat region 68327..68362
/note="18.0 copies 2 mer AC 27% conserved"

repeat region 68364..68373
/note="2.5 copies 4 mer CATG 20% conserved"

repeat region 68405..68415

repeat region /note="2.2 copies 5 mer ACAA 22% conserved"
68443..68453

repeat region /note="2.2 copies 5 mer AGGAA 22% conserved"
69224..69233

repeat region /note="2.5 copies 4 mer TATG 20% conserved"
69387..69396

repeat region /note="2.5 copies 4 mer CAAG 20% conserved"
69403..69415

repeat region /note="2.2 copies 6 mer AGAACA 26% conserved"
69603..69613

repeat region /note="2.8 copies 4 mer CTTC 22% conserved"
69620..69847

repeat region /note="MLT1L repeat: matches 362..614 of consensus"
69906..69916

repeat region /note="11.0 copies 1 mer T 22% conserved"
complement(69941..70137)

repeat region /note="L1MA4 repeat: matches 6105..6300 of consensus"
70144..70156

repeat region /note="2.2 copies 6 mer CTTTGT 26% conserved"
70242..70256

repeat region /note="5.0 copies 3 mer ATA 21% conserved"
complement(70306..70409)

repeat region /note="MIR repeat: matches 20..145 of consensus"
70488..71104

misc feature /note="match: GSS: Em:AG054326"

repeat region 70763..70970

repeat region /note="MIR repeat: matches 7..231 of consensus"
complement(71093..71538)

repeat region /note="MLT1H repeat: matches 61..522 of consensus"
71160..71170

repeat region /note="2.8 copies 4 mer GTTG 22% conserved"
71237..71246

repeat region /note="2.5 copies 4 mer TGGC 20% conserved"
71319..71328

repeat region /note="3.3 copies 3 mer CTC 20% conserved"
71462..71476

repeat region /note="3.0 copies 5 mer CCCAG 21% conserved"
71697..71718

repeat region /note="5.5 copies 4 mer TTGT 28% conserved"
71698..71720

repeat region /note="3.8 copies 6 mer TGTTTG 30% conserved"
71997..72007

repeat region /note="2.2 copies 5 mer GCCAG 22% conserved"
72980..73015

repeat region /note="6.0 copies 6 mer CCCC GC 45% conserved"
73221..73231

repeat region /note="2.8 copies 4 mer AGAA 22% conserved"
73694..73716

repeat region /note="11.5 copies 2 mer CA 37% conserved"
73726..73736

repeat region /note="2.2 copies 5 mer TGGAT 22% conserved"
73737..73748

repeat region /note="2.0 copies 6 mer CCCAAG 24% conserved"
73832..73842

repeat region /note="2.8 copies 4 mer GGGA 22% conserved"
74777..74788

repeat region /note="3.0 copies 4 mer TGGC 24% conserved"
75004..75017

repeat region /note="3.5 copies 4 mer GGGA 28% conserved"
75333..75357

repeat region /note="25.0 copies 1 mer A 50% conserved"
75705..75715

repeat region /note="3.7 copies 3 mer CTC 22% conserved"
76973..77273

repeat region /note="AluSx repeat: matches 1..298 of consensus"

<u>repeat region</u>	77258..77273 /note="16.0 copies 1 mer A 32% conserved"
<u>misc feature</u>	77384..77797 /note="match: GSS: Em:AQ237590"
<u>repeat region</u>	77399..77599 /note="MER20 repeat: matches 1..218 of consensus"
<u>repeat region</u>	77714..77727 /note="2.3 copies 6 mer TACTTT 28% conserved"
<u>repeat region</u>	78125..78136 /note="2.4 copies 5 mer TTGTC 24% conserved"
<u>repeat region</u>	78258..78269 /note="2.0 copies 6 mer TTATTC 24% conserved"
<u>repeat region</u>	78968..78989 /note="2.8 copies 8 mer AAAGAAAA 35% conserved"
<u>repeat region</u>	79074..79286 /note="L1ME1 repeat: matches 4184..4392 of consensus"
<u>repeat region</u>	79287..79572 /note="AluJb repeat: matches 3..306 of consensus"
<u>repeat region</u>	79476..79488 /note="2.2 copies 6 mer GAGGCT 26% conserved"
<u>repeat region</u>	79549..79572 /note="24.0 copies 1 mer A 21% conserved"
<u>repeat region</u>	79551..79575 /note="4.2 copies 6 mer AAAAAC 43% conserved"
<u>repeat region</u>	79552..79571 /note="4.0 copies 5 mer AAAAC 31% conserved"
<u>repeat region</u>	79573..79926 /note="L1ME1 repeat: matches 4392..4760 of consensus"
<u>repeat region</u>	79642..79652 /note="2.8 copies 4 mer GAAA 22% conserved"
<u>repeat region</u>	79800..79813 /note="2.3 copies 6 mer CTGACT 28% conserved"
<u>repeat region</u>	79933..80076 /note="L1ME1 repeat: matches 5148..5306 of consensus"
<u>repeat region</u>	80092..80105 /note="2.3 copies 6 mer ATTTTT 28% conserved"
<u>repeat region</u>	80103..80114 /note="6.0 copies 2 mer TA 24% conserved"
<u>repeat region</u>	complement(80117..80382) /note="AluJo repeat: matches 35..288 of consensus"
<u>repeat region</u>	80283..80295 /note="2.6 copies 5 mer TTTAT 26% conserved"
<u>repeat region</u>	80383..80400 /note="18.0 copies 1 mer A 27% conserved"
<u>repeat region</u>	80404..80421 /note="2.2 copies 8 mer AATTTT 36% conserved"
<u>repeat region</u>	80433..81196 /note="L1ME1 repeat: matches 5325..6148 of consensus"
<u>repeat region</u>	80691..80702 /note="3.0 copies 4 mer TTAA 24% conserved"
<u>repeat region</u>	81117..81130 /note="4.7 copies 3 mer GTG 28% conserved"
<u>misc feature</u>	81225..81678 /note="match: GSS: Em:AQ667566"
<u>repeat region</u>	81241..81445 /note="MER3 repeat: matches 1..208 of consensus"
<u>repeat region</u>	81369..81386 /note="3.6 copies 5 mer TTTCA 27% conserved"
<u>repeat region</u>	81382..81401 /note="2.0 copies 10 mer AATTAACTG 31% conserved"
<u>repeat region</u>	81416..81430 /note="2.1 copies 7 mer TAGCTAC 30% conserved"
<u>repeat region</u>	81584..81881 /note="AluSx repeat: matches 1..300 of consensus"
<u>repeat region</u>	81791..81802

repeat region /note="2.0 copies 6 mer CAGAGG 24% conserved"
81864..81881
repeat region /note="18.0 copies 1 mer A 36% conserved"
82185..82207
repeat region /note="1.9 copies 12 mer AAGAAAATACAC 37% conserved"
82374..82682
repeat region /note="AluJo repeat: matches 4..301 of consensus"
82664..82682
repeat region /note="19.0 copies 1 mer A 38% conserved"
82914..82923
repeat region /note="2.5 copies 4 mer ATGT 20% conserved"
83196..83772
repeat region /note="HAL1 repeat: matches 780..1357 of consensus"
83702..83716
repeat region /note="3.8 copies 4 mer AAAT 21% conserved"
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repeat region /note="HAL1 repeat: matches 1417..1762 of consensus"

ORIGIN

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